```
          10                  30                  50
TTCGGGCACGAGGGCAGGATGGCGCCACCACCAGCTAGAGTACATCTAGGTGCGTTCCTG
                    M  A  P  P  P  A  R  V  H  L  G  A  F  L
          70                  90                  110
GCAGTGACTCCGAATCCCGGGAGCGCAGCGAGTGGGACAGAGGCAGCCGCGGCCACACCC
A  V  T  P  N  P  G  S  A  A  S  G  T  E  A  A  A  A  T  P
         130                 150                 170
AGCAAAGTGTGGGGCTCTTCCGCGGGGAGGATTGAACCACGAGGCGGGGGCCGAGGAGCG
S  K  V  W  G  S  S  A  G  R  I  E  P  R  G  G  G  R  G  A
         190                 210                 230
CTCCCTACCTCCATGGGACAGCACGGACCCAGTGCCCGGGCCCGGGCAGGGCGCGCCCCA
L  P  T  S  M  G  Q  H  G  P  S  A  R  A  R  A  G  R  A  P
         250                 270                 290
GGACCCAGGCCGGCGCGGGAAGCCAGCCCTCGGCTCCGGGTCCACAAGACCTTCAAGTTT
G  P  R  P  A  R  E  A  S  P  R  L  R  V  H  K  T  F  K  F
         310                 330                 350
GTCGTCGTCGGGGTCCTGCTGCAGGTCGTACCTAGCTCAGCTGCAACCATCAAACTTCAT
V  V  V  G  V  L  L  Q  V  V  P  S  S  A  A  T  I  K  L  H
         370                 390                 410
GATCAATCAATTGGCACACAGCAATGGGAACATAGCCCTTTGGGAGAGTTGTGTCCACCA
D  Q  S  I  G  T  Q  Q  W  E  H  S  P  L  G  E  L  C  P  P
         430                 450                 470
GGATCTCATAGATCAGAACGTCCTGGAGCCTGTAACCGGTGCACAGAGGGTGTGGGTTAC
G  S  H  R  S  E  R  P  G  A  C  N  R  C  T  E  G  V  G  Y
         490                 510                 530
ACCAATGCTTCCAACAATTTGTTTGCTTGCCTCCCATGTACAGCTTGTAAATCAGATGAA
T  N  A  S  N  N  L  F  A  C  L  P  C  T  A  C  K  S  D  E
         550                 570                 590
GAAGAGAGAAGTCCCTGCACCACGACCAGGAACACAGCATGTCAGTGCAAACCAGGAACT
E  E  R  S  P  C  T  T  T  R  N  T  A  C  Q  C  K  P  G  T
         610                 630                 650
TTCCGGAATGACAATTCTGCTGAGATGTGCCGGAAGTGCAGCACAGGGTGCCCCAGAGGG
F  R  N  D  N  S  A  E  M  C  R  K  C  S  T  G  C  P  R  G
         670                 690                 710
ATGGTCAAGGTCAAGGATTGTACGCCCTGGAGTGACATCGAGTGTGTCCACAAAGAATCA
M  V  K  V  K  D  C  T  P  W  S  D  I  E  C  V  H  K  E  S
```

FIG.1A

```
        730                 750                 770
GGCAATGGACATAATATATGGGTGATTTTGGTTGTGACTTTGGTTGTTCCGTTGCTGTTG
G  N  G  H  N  I  W  V  I  L  V  V  T  L  V  V  P  L  L  L
                  **********************************************

        790                 810                 830
GTGGCTGTGCTGATTGTCTGTTGTTGCATCGGCTCAGGTTGTGGAGGGGACCCCAAGTGC
V  A  V  L  I  V  C  C  C  I  G  S  G  C  G  G  D  P  K  C
**************************************

        850                 870                 890
ATGGACAGGGTGTGTTTCTGGCGCTTGGGTCTCCTACGAGGGCCTGGGGCTGAGGACAAT
M  D  R  V  C  F  W  R  L  G  L  L  R  G  P  G  A  E  D  N
        910                 930                 950
GCTCACAACGAGATTCTGAGCAACGCAGACTCGCTGTCCACTTTCGTCTCTGAGCAGCAA
A  H  N  E  I  L  S  N  A  D  S  L  S  T  F  V  S  E  Q  Q
        970                 990                 1010
ATGGAAAGCCAGGAGCCGGCAGATTTGACAGGTGTCACTGTACAGTCCCCAGGGGAGGCA
M  E  S  Q  E  P  A  E  L  T  G  V  T  V  Q  S  P  G  E  A
        1030                1050                1070
CAGTGTCTGCTGGGACCGGCAGAAGCTGAAGGGTCTCAGAGGAGGAGGCTGCTGGTTCCA
Q  C  L  L  G  P  A  E  A  E  G  S  Q  R  R  R  L  L  V  P
        1090                1110                1130
GCAAATGGTGCTGACCCCACTGAGACTCTGATGCTGTTCTTTGACAAGTTTGCAAACATC
A  N  G  A  D  P  T  E  T  L  M  L  F  F  D  K  F  A  N  I
        1150                1170                1190
GTGCCCTTTGACTCCTGGGACCAGCTCATGAGGCAGCTGGACCTCACGAAAAATGAGATC
V  P  F  D  S  W  D  Q  L  M  R  Q  L  D  L  T  K  N  E  I
        1210                1230                1250
GATGTGGTCAGAGCTGGTACAGCAGGCCCAGGGGATGCCTTGTATGCAATGCTGATGAAA
D  V  V  R  A  G  T  A  G  P  G  D  A  L  Y  A  M  L  M  K
        1270                1290                1310
TGGGTCAACAAAACTGGACGGAACGCCTCGATCCACACCCTGCTGGATGCCTTGGAGAGG
W  V  N  K  T  G  R  N  A  S  I  H  T  L  L  D  A  L  E  R
        1330                1350                1370
ATGGAAGAGAGACATGCAAAAGAGAAGATTCAGGACCTCTTGGTGGACTCTGGAAAGTTC
M  E  E  R  H  A  K  E  K  I  Q  D  L  L  V  D  S  G  K  F
```

FIG.1B

```
      1390                1410                1430
ATCTACTTAGAAGATGGCACAGGCTCTGCCGTGTCCTTGGAGTGAAAGACTCTTTTTACC
I  Y  L  E  D  G  T  G  S  A  V  S  L  E
      1450                1470                1490
AGAGGTTTCCTCTTAGGTGTTAGGAGTTAATACATATTAGGTTTTTTTTTTTTTTAACAT
      1510                1530                1550
GTATACAAAGTAAATTCTTAGCCACGTGTATTGGCTCCTGCCTGTAATCCCATCACTTTG
      1570                1590                1610
GGAGGCTGACGCCGGTGGATCCACTTGAGGTCCGAAGTTCCAAGACCAGCCCTGAACCAA
      1630                1650                1670
CATCGTGGAAATGCCCGTCTTTTACAAAAAAATACCAAAAATTCAACTGGAATGTGCATG
      1690                1710                1730
GTGTGTGCCATCATTTCCTCGGCTAACTACGGGAGGTCTGAGGCCAGGAGAATCCACTTG
      1750                1770                1790
AACCCCACGAAGGACAGTGTAGACTGCAGATTGCACCACTGCACTCCCAGCCTGGGAACA
      1810                1830                1850
CAGAGCAAGACTCTGTCTCAAGATAAAATAAAATAAACTTGAAAGAATTATTGCCCGACT
      1870                1890                1910
GAGGCTCACATGCCAAAGGAAAATCTGGTTCTCCCCTGAGCTGGCCTCCGTGTGTTTCCT
      1930                1950                1970
TATCATGGTGGTCAATTGGAGGTGTTAATTTGAATGGATTAAGGAACACCTAGAACACTG
      1990                2010                2030
GTAAGGCATTATTTCTGGGACATTATTTCTGGGCATGTCTTCGAGGGTGTTTCCAGAGGG
      2050                2070                2090
GATTGGCATGCGATCGGGTGGACTGAGTGGAAAAGACCTACCCTTAATTTGGGGGGGCAC
      2110                2130                2150
CGTCCGACAGACTGGGGAGCAAGATAGAAGAAAACAAAAAAAAAAAAAAAAA
```

FIG.1C

```
1   M---------LG-------------------------IWT-  h Fas protein
1   MGLSTVPDLLLPLVLLELLVGIYPSGVIGLVPH-------  h TNFR I Protein
1   MEQRPRGCAAVAAALLLVLLGARAQG--------------  DR3 protein
1   MAPPPARVHLGAFLAVTPNPGSAASGTEAAAATPSKVWGS  DR4 protein

7   ----------------LLPLVLT---SV------ARL-SSKSVN  h Fas protein
34  -LGDREKRDSVCPQGKYIHPQNNSICCTKCHKGTYLYNDC  h TNFR I Protein
27  --GTRSPR-CDCA-GDF-HKKIGLFCCRGCPAGHYLKAPC  DR3 protein
41  SAGRIEPRGGGRGALPTSMGQHGPS------ARARAGRAPG  DR4 protein

25  AQVTDINSKGLELRKTVTTVETQNLEG-----------LHH  h Fas protein
73  PGPGQDTDCRECESGSFTASENHLR-HCLSCSKCRKEMGQ  h TNFR I Protein
62  TEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQ  DR3 protein
76  PRPAREASPRLRVHKTFKFVVVGVLLQVVPSSAATIKLHD  DR4 protein

55  DG----QFCHKP----CPPGERKARDCTVNGDEPDCVPCQ  h Fas protein
112 VEISS----------CTVDRDTVCGC----RKNQYRHYW  h TNFR I Protein
102 VALEN----------CSAVADTRCGC----KPGWFVEC-  DR3 protein
116 QSIGTQQWEHSPLGELCPPGSHRS------ERPGACNRCT  DR4 protein

87  EGKEYTDKAHFSSKCRRCRLCDEGHGLEVEINCTRTQNTK  h Fas protein
137 SENLFQC-----FNCSLCLN-GTVH-----LSCQEKQNTV  h TNFR I Protein
126 --QVSQCVSSSPFYCQPCLDCGALHR-HTRLLCSRRDTDC  DR3 protein
150 EGVGYTNASNNLFACLPCTACKSDE--EERSPCTTTRNTA  DR4 protein
```

FIG.2A

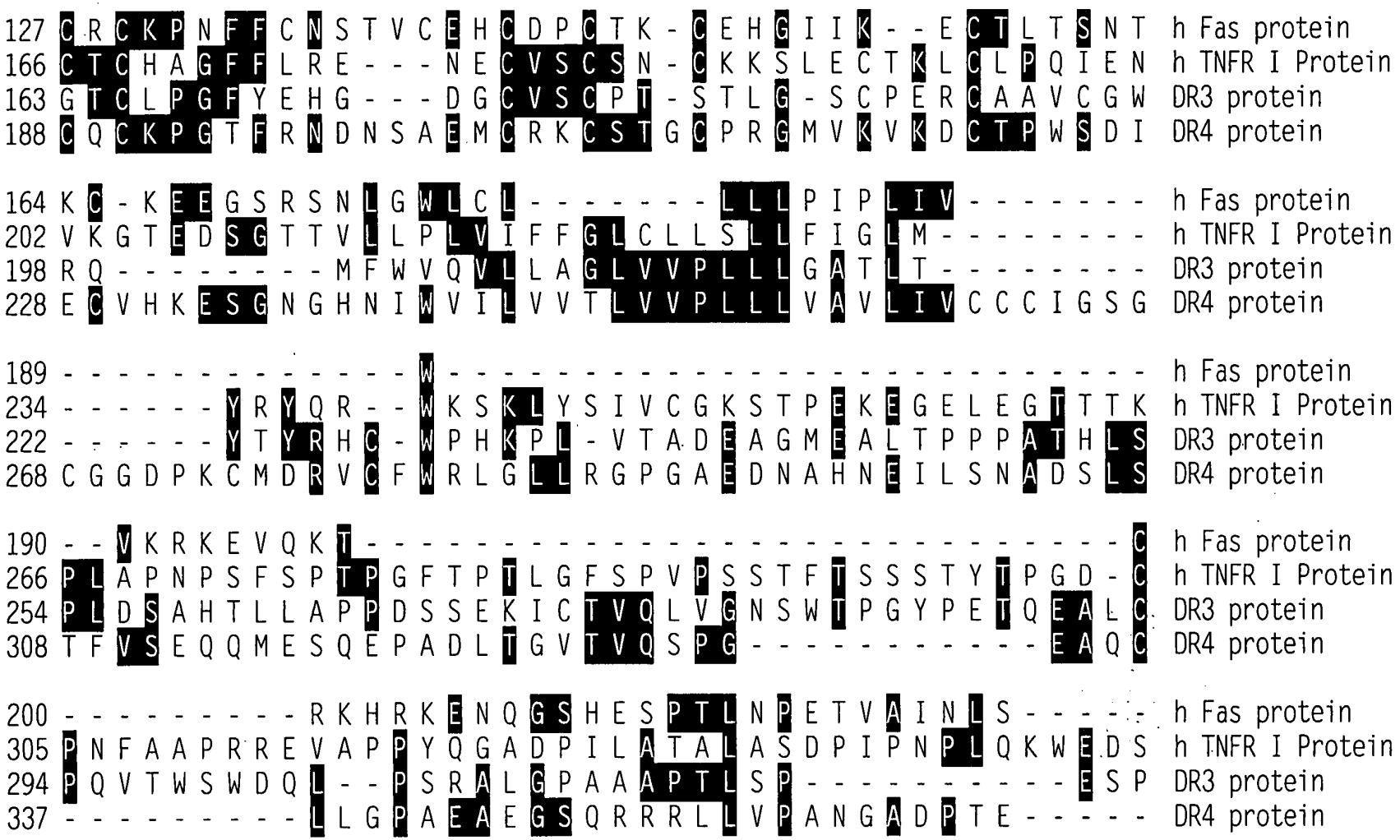

FIG.2B

```
226 ---------DVDLSKYITTIAGVMTLSQVKGFVRKNGVNEA  h Fas protein
345 AHKPQSLDTDDPATLYAVVENVPPL-RWKEFVRRLGLSDH  h TNFR I Protein
322 AGSPAMMLQPGPQ-LYDVMDAVPAR-RWKEFVRTLGLREA  DR3 protein
363 ---------TLML--FFDKFANIVPFDSWDQLMRQLDLTKN  DR4 protein

258 KIDEIKNDNVQDTAEQKVQLLRNWHQLHGKKEA-YDTLIK  h Fas protein
384 EIDRLELQNGRCLREAQYSMLATWRRRTPRREATLELLGR  h TNFR I Protein
360 EIEAVEVEIGR-FRDQQYEMLKRWRQQQP---AGLGAVYA  DR3 protein
393 EIDVVRAGTA-GPGDALYAMLMKWVNKTGRNAS-IHTLLD  DR4 protein

297 DLKKANLCTLAEKIQTIILKDITSDSENSNFRNEIQSLV   h Fas protein
424 VLRDMDLLGCLEDIEEAL--------CGPAALPPAPSLLR  h TNFR I Protein
396 ALERMGLDGCVEDL----------------RSRLQRGP    DR3 protein
431 ALERMEERHAKEKIQDLLVDSGKFIYLEDGTGSAVSLE    DR4 protein
```

FIG.2C

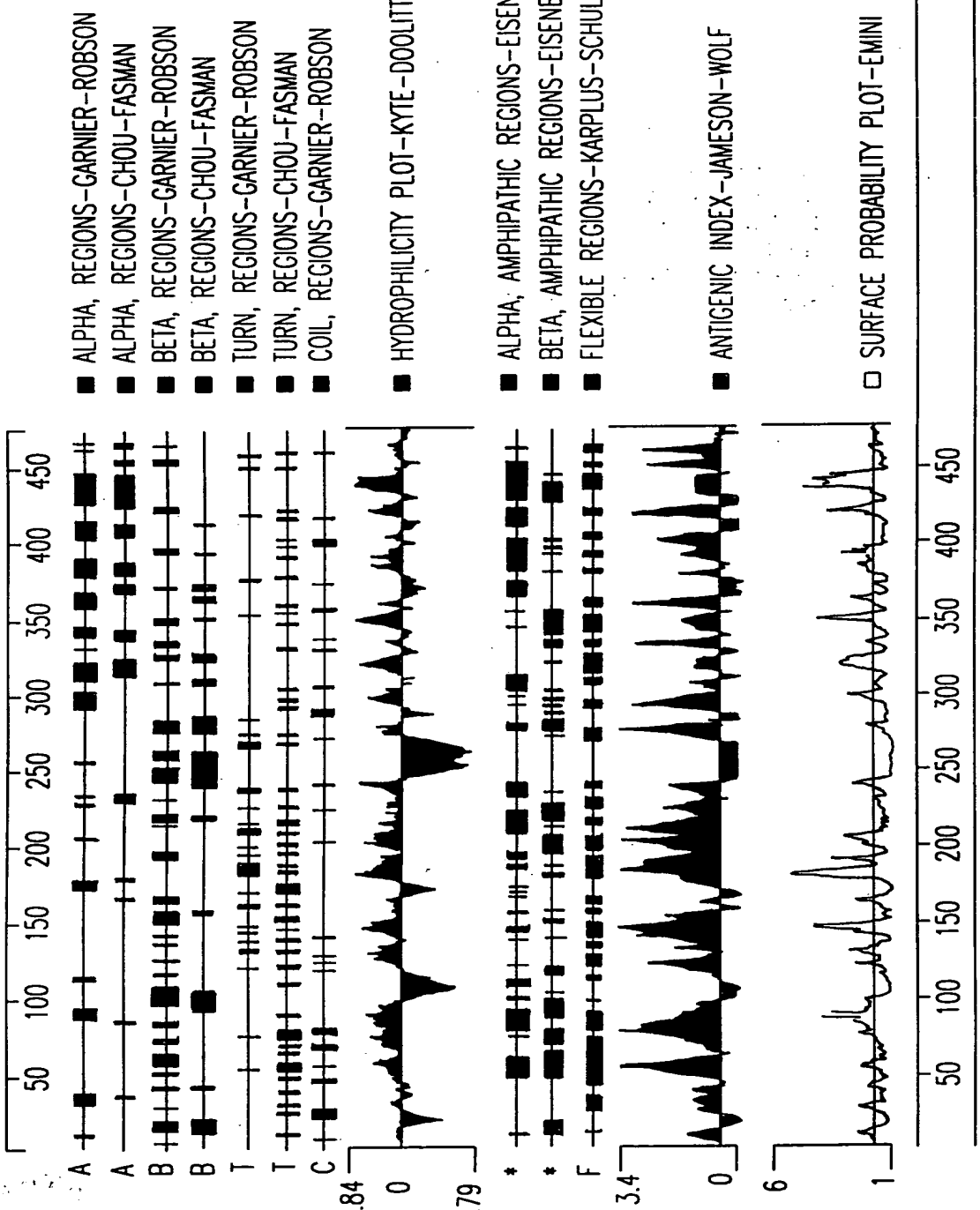

FIG.3

HTOIY07R

```
  1  GGCANAGGTN CGTACCTAGC TCACCTGCAA CCATCAAACT TNATGATCAA
 51  TCAATTGGCA CACAGCAATG GGAAACATAG CCCTTTGGAA GANTTGTNTC
101  CACCAGGATC TCATAGATCA AAACATCCTG GGAGCCTGTT AACCGGTGCC
151  CCAAAGGNTG GTCAAGGTCA AGGAATTGTT NCGCCCTGGA AGTGAACATC
201  GAGTGTNTCC ACAAAGGATT CAGGCAATGG GACATAAATA TATGGGTGAA
251  TTTTGGTTGT GAACTTTGGT TGNTCCCGTT GNTGTTGNTG GCTGTGCTGA
301  TTGTTTGTTG TTGCATCGGC TTCAGGTTNT GGAGGGGGAC CCAAGTGCAT
351  GGACAGGGTG TGTTTCTGGG GTTTGGGTCT CTTAGAGGGC NTGGGTTANG
401  GCANGTTCAC AAGGGTTTTA GCAANG
```

HTXEY80R

```
  1  TGGGGCTGAG GACAATGCTG ACNACGAGAT TCTGAGCAAC GCAGNACTNG
 51  CTGTCCACTT TCGTCTNTGN GCAGCAAATG GAAAGCCAGG AGCCGGCAGA
101  TTTGACAGGT GTCACTGTAC AGTCCCCAGG GGAGGCACAG TGTCTGCTGG
151  TGAGTTGGGG ACAGGCCCTT GCAAGACCTT GTGAGGCAGG GGGTGAAGGC
201  CATGNCTCGG CTTCNNNTGG TCAAAGGGGA AGTGGAGCCT GAGGGAGATG
251  GGACTTNAGG GGGACGGNGC TGCGTGGGGA AAAAGCAGCC ACCNTTTGAC
301  AAGGGGGACA GGCATTTTTN CAAATGTGTG CTTNTTGGT
```

FIG.4

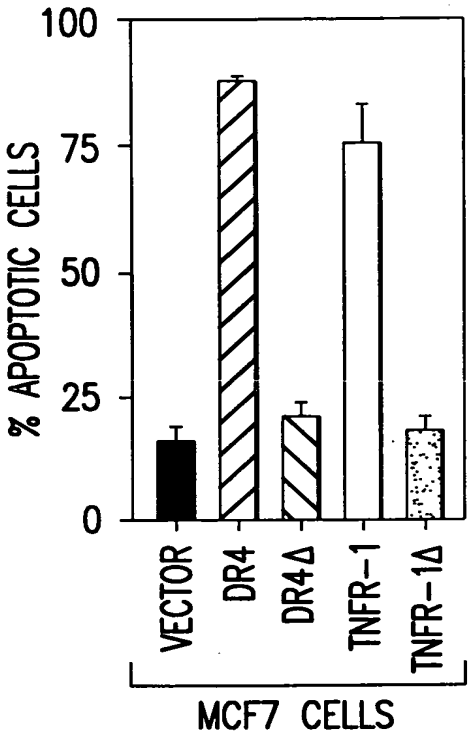

FIG.5A

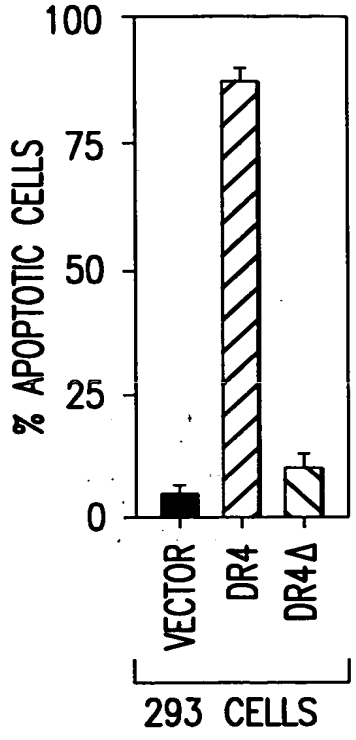

FIG.5B

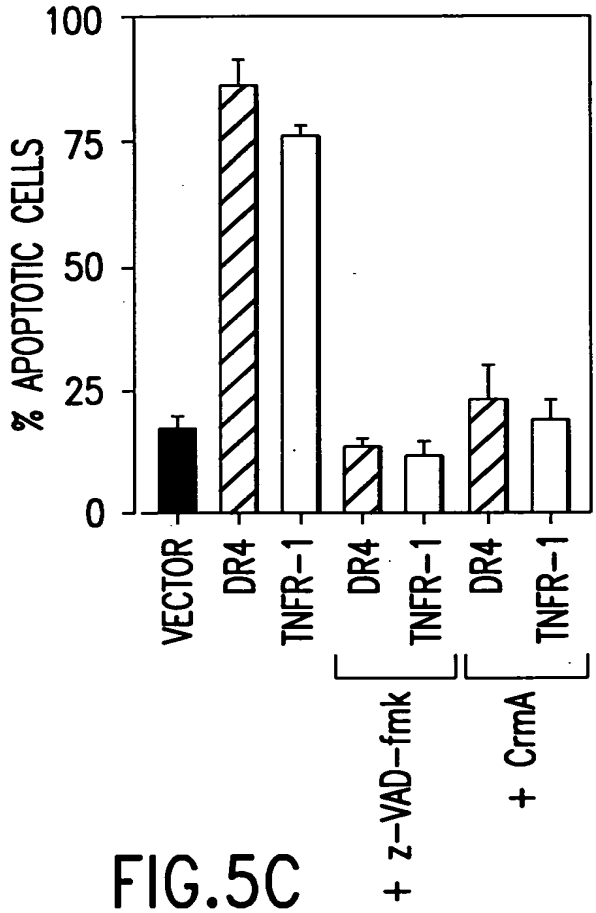

FIG.5C

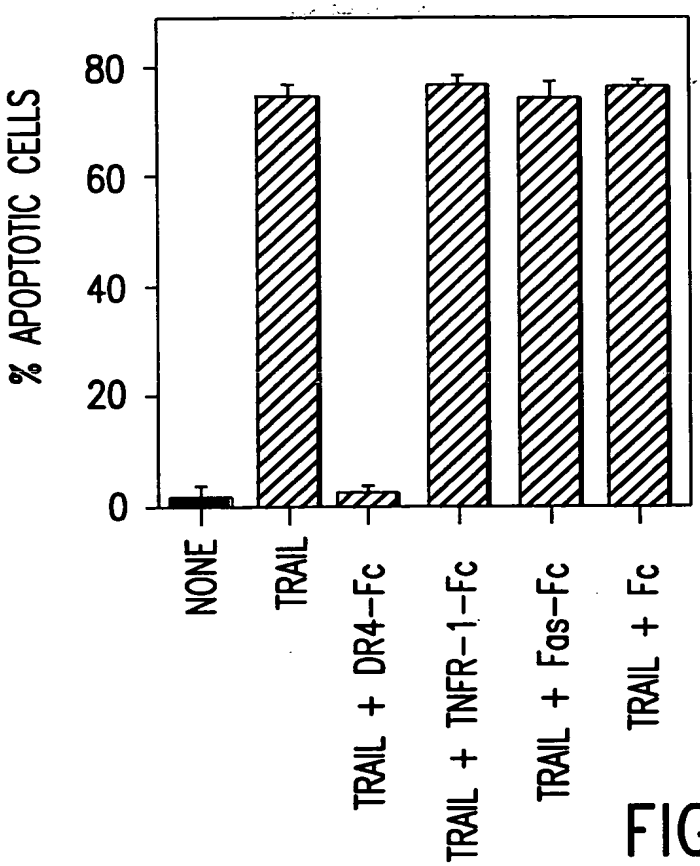

FIG.6A

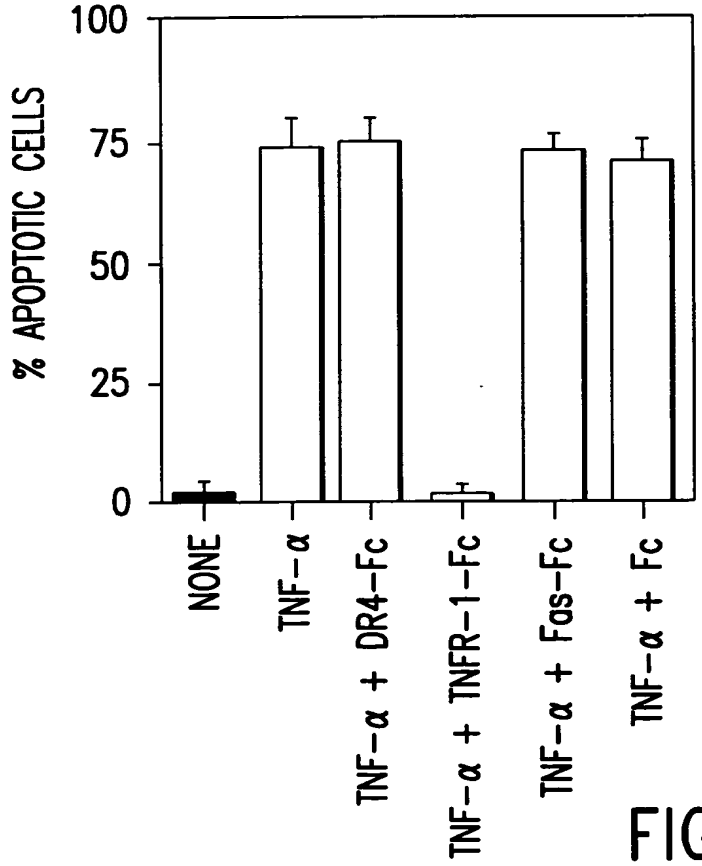

FIG.6B